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results of **BLAST**

## BLASTN 2.2.6 [Apr-09-2003]

RID: 1067965636-22392-2125968.BLASTQ3

Query=

5  
(2213 letters)

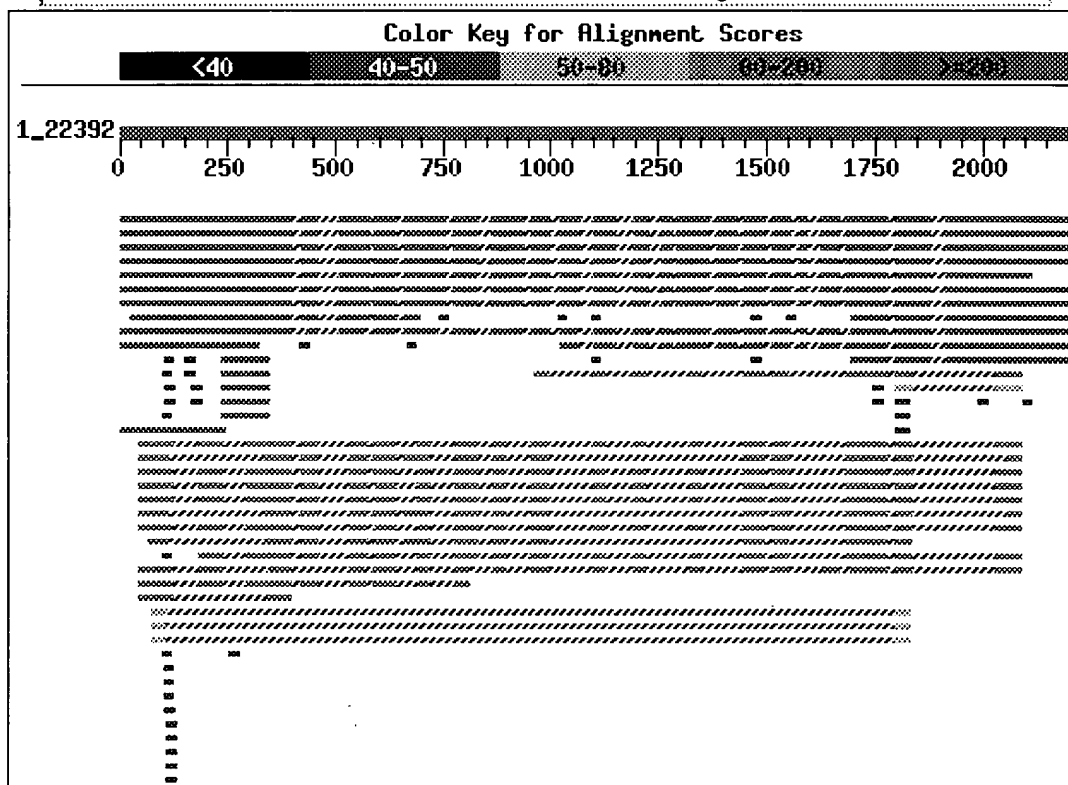
**Database:** All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)

1,962,268 sequences; 9,398,544,397 total letters

Taxonomy reports

### Distribution of 530 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:

Score E  
(bits) Value

<a href="#">gi 7264728 gb AF231121.1 AF231121</a>	Homo sapiens iron-regulat...	<a href="#">789</a>	0.0	
<a href="#">gi 7109248 gb AF226614.1 AF226614</a>	Homo sapiens ferroportin1...	<a href="#">789</a>	0.0	
<a href="#">gi 8895484 gb AF215636.1 AF215636</a>	Homo sapiens SLC11A3 iron...	<a href="#">789</a>	0.0	

gi 23273531 gb BC035893.1	Homo sapiens solute carrier fami...	775	0.0	100
gi 12053382 emb AL136944.1 HSM801908	Homo sapiens mRNA; cDN...	775	0.0	100
gi 22902429 gb BC037733.1	Homo sapiens solute carrier fami...	759	0.0	100
gi 31543639 ref NM_014585.3	Homo sapiens solute carrier fa...	759	0.0	100
gi 33337961 gb AF171087.1	Homo sapiens MSTP079 (MST079) mR...	704	0.0	
gi 13270751 gb AC013439.11	Homo sapiens BAC clone RP11-270...	676	0.0	
gi 38043879 emb AJ604512.1	Homo sapiens partial SLC40A1 ge...	628	e-176	
gi 4761673 gb AF147322.1 AF147322	Homo sapiens full length ...	511	e-141	100
gi 31873559 emb BX537503.1 HSM805934	Homo sapiens mRNA; cDN...	504	e-139	
gi 7023677 dbj AK002038.1	Homo sapiens cDNA FLJ11176 fis, ...	504	e-139	100
gi 1034464 emb Z62086.1 HS63B9F	H.sapiens CpG island DNA ge...	228	3e-56	
gi 1028150 emb Z56919.1 HS153B8R	H.sapiens CpG island DNA g...	224	5e-55	
gi 1028149 emb Z56918.1 HS153B8F	H.sapiens CpG island DNA g...	222	2e-54	
gi 1028147 emb Z56916.1 HS153B7F	H.sapiens CpG island DNA g...	216	1e-52	
gi 1028148 emb Z56917.1 HS153B7R	H.sapiens CpG island DNA g...	210	8e-51	
gi 15880970 emb AJ336552.1 HSA336552	Homo sapiens genomic s...	206	1e-49	
gi 8394303 ref NM_016917.1	Mus musculus solute carrier fam...	167	1e-37	100
gi 18959259 ref NM_133315.1	Rattus norvegicus solute carri...	167	1e-37	100
gi 13097389 gb BC003438.1	Mus musculus solute carrier fami...	167	1e-37	100
gi 12843053 dbj AK008700.1	Mus musculus adult male stomach...	167	1e-37	100
gi 18846873 gb AF394785.3	Rattus norvegicus ferroportin 1 ...	167	1e-37	100
gi 26328524 dbj AK032732.1	Mus musculus 12 days embryo mal...	167	1e-37	100
gi 7264726 gb AF231120.1 AF231120	Mus musculus iron-regulat...	167	1e-37	100
gi 7109246 gb AF226613.1 AF226613	Mus musculus ferroportin1...	167	1e-37	100
gi 4098298 gb U76714.1 RRU76714	Rattus norvegicus cell adhe...	167	1e-37	100
gi 8895486 gb AF215637.1 AF215637	Mus musculus SLC11A3 iron...	167	1e-37	100
gi 28933915 gb AC123557.4	Mus musculus chromosome 1 clone ...	141	6e-30	
gi 26083702 dbj AK033987.1	Mus musculus adult male diencep...	107	9e-20	
gi 25990284 gb AF216834.2	Mus musculus ferroportin 1 (Slc3...	101	5e-18	100
gi 26350408 dbj AK083288.1	Mus musculus adult male liver t...	74	1e-09	100
gi 18859378 ref NM_131629.1	Danio rerio solute carrier fam...	52	0.004	100
gi 19309470 emb AL591593.11	Zebrafish DNA sequence from cl...	52	0.004	100
gi 7109244 gb AF226612.1 AF226612	Danio rerio ferroportin1 ...	52	0.004	100
gi 37591194 gb AC145321.2	Oryza sativa chromosome 11 BAC c...	46	0.27	
gi 20146016 emb AL672145.5	Zebrafish DNA sequence from clo...	46	0.27	100
gi 21998245 emb AL731861.9	Zebrafish DNA sequence from clo...	46	0.27	100
gi 21212284 emb AL672118.8	Zebrafish DNA sequence from clo...	46	0.27	100
gi 32984852 dbj AK099643.1	Oryza sativa (japonica cultivar...	46	0.27	
gi 37651897 gb AC146048.3	Pan troglodytes BAC clone RP43-4...	44	1.1	
gi 4508108 gb AC005101.2	Homo sapiens BAC clone CTA-352J5 ...	44	1.1	
gi 20564430 gb AC044786.3	Homo sapiens chromosome 10 clone...	44	1.1	
gi 15149567 emb AL512366.12	Human DNA sequence from clone ...	44	1.1	100
gi 34531610 dbj AK125496.1	Homo sapiens cDNA FLJ43507 fis,...	44	1.1	
gi 32398496 emb BX294670.6	Zebrafish DNA sequence from clo...	44	1.1	
gi 14329082 gb AC011472.7 AC011472	Homo sapiens chromosome ...	44	1.1	
gi 6911646 emb AL109865.36 HSG120K12	Human DNA sequence fro...	44	1.1	100
gi 34330231 gb AC117573.9	Mus musculus chromosome 3, clone...	42	4.3	
gi 34849934 gb AC069562.51	Mus musculus clone rp23-317e13 ...	42	4.3	
gi 18416290 ref NM_118549.1	Arabidopsis thaliana hypotheti...	42	4.3	100
gi 28973809 gb AC092378.4	Homo sapiens chromosome 16 clone...	42	4.3	
gi 20976936 gb AF374874.1	Villanova achillaeoides internal...	42	4.3	

<a href="#">gi 4567137 gb AF134471.1 </a>	Homo sapiens chromosome 10 clone ...	<a href="#">42</a>	4.3
<a href="#">gi 21536172 gb AC121772.2 </a>	Mus musculus clone RP23-349L11, ...	<a href="#">42</a>	4.3
<a href="#">gi 21070776 gb AC115621.3 </a>	Homo sapiens BAC clone RP11-315D...	<a href="#">42</a>	4.3
<a href="#">gi 20514812 gb AC012468.10 </a>	Homo sapiens chromosome 10 clon...	<a href="#">42</a>	4.3
<a href="#">gi 23496930 gb AE014851.1 </a>	Plasmodium falciparum 3D7 chromo...	<a href="#">42</a>	4.3
<a href="#">gi 12666243 emb AL354802.15 </a>	Human DNA sequence from clone ...	<a href="#">42</a>	4.3
<a href="#">gi 26801347 gb AC124742.4 </a>	Mus musculus chromosome 12 clone...	<a href="#">42</a>	4.3
<a href="#">gi 15145546 gb AC019064.6 </a>	Homo sapiens BAC clone RP11-1530...	<a href="#">42</a>	4.3
<a href="#">gi 24413714 emb AL939104.1 </a>	SCO939104 Streptomyces coelicolo...	<a href="#">42</a>	4.3
<a href="#">gi 25815290 gb AC012183.9 </a>	Homo sapiens chromosome 16 clone...	<a href="#">42</a>	4.3
<a href="#">gi 7269265 emb AL161561.2 </a>	ATCHRIV61 Arabidopsis thaliana DN...	<a href="#">42</a>	4.3
<a href="#">gi 5668629 emb AL109619.1 </a>	ATT19F6 Arabidopsis thaliana DNA ...	<a href="#">42</a>	4.3
<a href="#">gi 16413128 emb AL596166.1 </a>	Listeria innocua Clip11262 comp...	<a href="#">42</a>	4.3
<a href="#">gi 11125649 emb AL121775.3 </a>	CNS01DSG Human chromosome 14 DNA...	<a href="#">42</a>	4.3
<a href="#">gi 6249674 gb AC005874.3 </a>	AC005874 citb_175_g_20, complete s...	<a href="#">42</a>	4.3
<a href="#">gi 12484331 gb AC021667.21 </a>	AC021667 Mus musculus, clone RP2...	<a href="#">42</a>	4.3
<a href="#">gi 22474414 emb AL732296.11 </a>	Mouse DNA sequence from clone ...	<a href="#">42</a>	4.3
<a href="#">gi 9280718 gb AC068812.13 </a>	AC068812 Homo sapiens chromosome ...	<a href="#">42</a>	4.3
<a href="#">gi 2262097 gb AC002343.1 </a>	ATAC002343 Arabidopsis thaliana ch...	<a href="#">42</a>	4.3

## Alignments

Get selected sequences

Select all

Deselect all

☒ >[gi|7264728|gb|AF231121.1|AF231121](#)  Homo sapiens iron-regulated transporter complete cds  
Length = 2443

Score = 789 bits (398), Expect = 0.0  
Identities = 398/398 (100%)  
Strand = Plus / Plus

Query: 1 agctggctcagggcggtccgctaggctcggacgacctgctgagcctcccaaaccgcttcca 60  
|||||  
Sbjct: 1 agctggctcagggcggtccgctaggctcggacgacctgctgagcctcccaaaccgcttcca 60

Query: 61 taaggctttgctttccaacttcagctacagtgttagctaagtttgaaagaaggaaaaaa 120  
|||||  
Sbjct: 61 taaggctttgctttccaacttcagctacagtgttagctaagtttgaaagaaggaaaaaa 120

Query: 121 gaaaatccctgggccccttttctttgttctttgccaagtcgctggttagtctttttg 180  
|||||  
Sbjct: 121 gaaaatccctgggccccttttctttgttctttgccaagtcgctggttagtctttttg 180

Query: 181 cccaaggctgttggttttagaggtgctatctccagttccttgcaactcctgttaacaag 240  
|||||  
Sbjct: 181 cccaaggctgttggttttagaggtgctatctccagttccttgcaactcctgttaacaag 240

Query: 241 cacctcagcgagagcagcagcagcgatagcagccgcagaagagccagcggggtcgcttag 300  
|||||  
Sbjct: 241 cacctcagcgagagcagcagcagcgatagcagccgcagaagagccagcggggtcgcttag 300

Query: 301 tgtcatgaccagggcgaggagatcacaaccgccagagaggatgctgtggatccttggccga 360  
|||||  
Sbjct: 301 tgtcatgaccagggcgaggagatcacaaccgccagagaggatgctgtggatccttggccga 360

Query: 361 ctacctgacctctgcaaaattccttctctaccttggtc 398  
|||||  
Sbjct: 361 ctacctgacctctgcaaaattccttctctaccttggtc 398

Score = 511 bits (258), Expect = e-141  
Identities = 281/290 (96%), Gaps = 9/290 (3%)  
Strand = Plus / Plus

Query: 1916 aatactctgggaacaagctctttgcttgcggtcctgatgcaaaagaatttgcccaagtt 1975  
|||||  
Sbjct: 1934 aatactctgggaacaagctctttgcttgcggtcctgatgcaaaagaa-----gtt 1984

Query: 1976 aggaaggaaaatcaagcaaatacatctgttgtttgagacagtttaactgttgctatcctg 2035  
|||||  
Sbjct: 1985 aggaaggaaaatcaagcaaatacatctgttgtttgagacagtttaactgttgctatcctg 2044

Query: 2036 ttactagattatatagagcacatgtgcttattttgtactgcagaattccaataaatggct 2095  
|||||  
Sbjct: 2045 ttactagattatatagagcacatgtgcttattttgtactgcagaattccaataaatggct 2104

Query: 2096 ggggtgttttgctctgtttttaccacagctgtgccttgagaactaaaagctgtttaggaaa 2155  
|||||  
Sbjct: 2105 ggggtgttttgctctgtttttaccacagctgtgccttgagaactaaaagctgtttaggaaa 2164

Query: 2156 cctaagtcagcagaaattaactgattaatttcccttatgttgaggcatgg 2205  
|||||  
Sbjct: 2165 cctaagtcagcagaaattaactgattaatttcccttatgttgaggcatgg 2214

Score = 192 bits (97), Expect = 2e-45  
Identities = 97/97 (100%)  
Strand = Plus / Plus

Query: 1684 tgctgctagaatcggtctttggctcctttgatttaactgtgacacagttgctgcaagaaaa 1743  
|||||  
Sbjct: 1693 tgctgctagaatcggtctttggctcctttgatttaactgtgacacagttgctgcaagaaaa 1752

Query: 1744 tgtaattgaatctgaaagaggcattataaatggtgta 1780  
|||||  
Sbjct: 1753 tgtaattgaatctgaaagaggcattataaatggtgta 1789

Score = 113 bits (57), Expect = 1e-21  
Identities = 57/57 (100%)  
Strand = Plus / Plus

Query: 773 gattggattgttgttgttgcaggagaagacagaagcaaactagcaaatatgaatgcc 829  
|||||  
Sbjct: 773 gattggattgttgttgttgcaggagaagacagaagcaaactagcaaatatgaatgcc 829

Score = 101 bits (51), Expect = 5e-18  
Identities = 51/51 (100%)  
Strand = Plus / Plus

Query: 1445 tgtttgatcttgtgtgtgatctctgtattcatgcctggaagccccctggac 1495  
|||||  
Sbjct: 1451 tgtttgatcttgtgtgtgatctctgtattcatgcctggaagccccctggac 1501

Score = 95.6 bits (48), Expect = 3e-16  
Identities = 48/48 (100%)  
Strand = Plus / Plus

Query: 1385 ggtttggttcggacaggtctgatctcaggattggcacagctttcctgt 1432  
|||||  
Sbjct: 1406 ggtttggttcggacaggtctgatctcaggattggcacagctttcctgt 1453

Score = 95.6 bits (48), Expect = 3e-16  
Identities = 48/48 (100%)  
Strand = Plus / Plus

Query: 1022 aaagaagaggaaactgaattgaaacagctgaatttacacaaagatact 1069  
|||||  
Sbjct: 1022 aaagaagaggaaactgaattgaaacagctgaatttacacaaagatact 1069

Score = 95.6 bits (48), Expect = 3e-16  
Identities = 48/48 (100%)  
Strand = Plus / Plus

Query: 956 tggaaggtttaccagaaaaccccagctctagctgtgaaagctggtcctt 1003  
|||||  
Sbjct: 974 tggaaggtttaccagaaaaccccagctctagctgtgaaagctggtcctt 1021

Score = 95.6 bits (48), Expect = 3e-16  
Identities = 48/48 (100%)  
Strand = Plus / Plus

Query: 590 ctggtggtacagaatgtttcagtcacctgtgtggaatcatcctgatg 637  
|||||  
Sbjct: 590 ctggtggtacagaatgtttcagtcacctgtgtggaatcatcctgatg 637

Score = 95.6 bits (48), Expect = 3e-16  
Identities = 48/48 (100%)  
Strand = Plus / Plus

Query: 530 ggtgactgggtggacaagaatgctagacttaaagtggcccagacctcg 577  
|||||  
Sbjct: 542 ggtgactgggtggacaagaatgctagacttaaagtggcccagacctcg 589

Score = 83.8 bits (42), Expect = 1e-12  
Identities = 42/42 (100%)  
Strand = Plus / Plus

Query: 1515 acttgtccgtttctccttttgaagatatccgatcaaggttca 1556  
|||||  
Sbjct: 1500 acttgtccgtttctccttttgaagatatccgatcaaggttca 1541

Score = 81.8 bits (41), Expect = 5e-12  
Identities = 41/41 (100%)  
Strand = Plus / Plus

Query: 1627 tgaatctgtgcccataatctctgtcagtcctgctgtttgcag 1667  
|||||  
Sbjct: 1645 tgaatctgtgcccataatctctgtcagtcctgctgtttgcag 1685

Score = 79.8 bits (40), Expect = 2e-11  
Identities = 40/40 (100%)  
Strand = Plus / Plus

Query: 1798 acagaactccatgaactatcttcttgatcttctgcatttc 1837  
|||||  
Sbjct: 1789 acagaactccatgaactatcttcttgatcttctgcatttc 1828

Score = 77.8 bits (39), Expect = 8e-11  
Identities = 39/39 (100%)  
Strand = Plus / Plus

Query: 419 cattctctctctacttggggagatcggatgtggcacttt 457  
|||||  
Sbjct: 398 cattctctctctacttggggagatcggatgtggcacttt 436

Score = 73.8 bits (37), Expect = 1e-09  
Identities = 38/39 (97%)  
Strand = Plus / Plus

Query: 656 atggtttttcttacataaacatgagcttctgaccatgtac 694  
|||||  
Sbjct: 638 atggtttttcttacataaacatgarcttctgaccatgtac 676

Score = 69.9 bits (35), Expect = 2e-08  
Identities = 35/35 (100%)  
Strand = Plus / Plus

Query: 1195 caaccagcctgtgtttctggctggcatgggtcttg 1229  
|||||  
Sbjct: 1213 caaccagcctgtgtttctggctggcatgggtcttg 1247

Score = 65.9 bits (33), Expect = 3e-07  
Identities = 33/33 (100%)  
Strand = Plus / Plus

Query: 860 acaatacgaaggattgaccagttaaccaacatc 892  
|||||  
Sbjct: 830 acaatacgaaggattgaccagttaaccaacatc 862

Score = 60.0 bits (30), Expect = 2e-05  
Identities = 30/30 (100%)  
Strand = Plus / Plus

Query: 1295 actgtcctgggctttgactgcatcaccaca 1324  
|||||  
Sbjct: 1262 actgtcctgggctttgactgcatcaccaca 1291

Score = 60.0 bits (30), Expect = 2e-05  
Identities = 30/30 (100%)  
Strand = Plus / Plus

Query: 1103 gagccaaaaccctggagggaactcatcta 1132  
|||||  
Sbjct: 1070 gagccaaaaccctggagggaactcatcta 1099

Score = 48.1 bits (24), Expect = 0.069  
Identities = 24/24 (100%)  
Strand = Plus / Plus



Query: 1343 atgggaactgtagcttttacttgg 1366  
|||||  
Sbjct: 1367 atgggaactgtagcttttacttgg 1390

Score = 48.1 bits (24), Expect = 0.069  
Identities = 24/24 (100%)  
Strand = Plus / Plus

Query: 1325 tccatcctcagtattttgatggga 1348  
|||||  
Sbjct: 1322 tccatcctcagtattttgatggga 1345

Score = 46.1 bits (23), Expect = 0.27  
Identities = 23/23 (100%)  
Strand = Plus / Plus

Query: 914 tggaacttggtatccatgtgcgt 936  
|||||  
Sbjct: 935 tggaacttggtatccatgtgcgt 957

Score = 44.1 bits (22), Expect = 1.1  
Identities = 22/22 (100%)  
Strand = Plus / Plus

Query: 716 actgcaatcacaatccaaagg 737  
|||||  
Sbjct: 752 actgcaatcacaatccaaagg 773

Score = 44.1 bits (22), Expect = 1.1  
Identities = 22/22 (100%)  
Strand = Plus / Plus

Query: 695 atcctgatcatcactattgcaa 716  
|||||  
Sbjct: 704 atcctgatcatcactattgcaa 725

Score = 44.1 bits (22), Expect = 1.1  
Identities = 22/22 (100%)  
Strand = Plus / Plus

Query: 510 tctacgggctggtggtggcagg 531  
|||||  
Sbjct: 492 tctacgggctggtggtggcagg 513

Score = 42.1 bits (21), Expect = 4.3  
 Identities = 21/21 (100%)  
 Strand = Plus / Plus

Query: 1859 ggccacattatgtatttccga 1879  
 |||||  
 Sbjct: 1904 ggccacattatgtatttccga 1924

Score = 42.1 bits (21), Expect = 4.3  
 Identities = 21/21 (100%)  
 Strand = Plus / Plus

Query: 1838 gaagcttttggcttgctcgta 1858  
 |||||  
 Sbjct: 1856 gaagcttttggcttgctcgta 1876

Score = 42.1 bits (21), Expect = 4.3  
 Identities = 21/21 (100%)  
 Strand = Plus / Plus

Query: 1574 tctgctaattgtcccggag 1594  
 |||||  
 Sbjct: 1616 tctgctaattgtcccggag 1636

Score = 42.1 bits (21), Expect = 4.3  
 Identities = 21/21 (100%)  
 Strand = Plus / Plus

Query: 1262 gggtagcctacactcaggga 1282  
 |||||  
 Sbjct: 1292 gggtagcctacactcaggga 1312

Score = 42.1 bits (21), Expect = 4.3  
 Identities = 21/21 (100%)  
 Strand = Plus / Plus

Query: 1133 cttgaacatgagcaagagcct 1153  
 |||||  
 Sbjct: 1130 cttgaacatgagcaagagcct 1150

Score = 42.1 bits (21), Expect = 4.3  
 Identities = 21/21 (100%)  
 Strand = Plus / Plus

Query: 893 atgacatttggtccccagtc 913  
 |||||  
 Sbjct: 890 atgacatttggtccccagtc 910

Score = 42.1 bits (21), Expect = 4.3  
 Identities = 21/21 (100%)  
 Strand = Plus / Plus

Query: 735 gggttctcacttcctgctata 755  
 |||||  
 Sbjct: 684 gggttctcacttcctgctata 704

>gi|7109248|gb|AF226614.1|AF226614 Homo sapiens ferroportin1 (FPN1) mRNA, co  
 Length = 2222

Score = 789 bits (398), Expect = 0.0  
 Identities = 398/398 (100%)  
 Strand = Plus / Plus

Query: 1 agctggctcagggcgctccgctaggctcggacgacctgctgagcctcccaaaccgcttcca 60  
 |||||  
 Sbjct: 1 agctggctcagggcgctccgctaggctcggacgacctgctgagcctcccaaaccgcttcca 60

Query: 61 taaggctttgctttccaacttcagctacagtgttagctaagtttgaaagaaggaaaaaa 120  
 |||||  
 Sbjct: 61 taaggctttgctttccaacttcagctacagtgttagctaagtttgaaagaaggaaaaaa 120

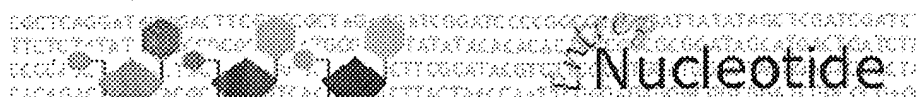
Query: 121 gaaaatccctgggccccttttcttttgttctttgccaaagtcgctcgttgtagtctttttg 180  
 |||||  
 Sbjct: 121 gaaaatccctgggccccttttcttttgttctttgccaaagtcgctcgttgtagtctttttg 180

Query: 181 cccaaggctgttggtgttttagaggtgctatctccagttccttgcaactcctgttaacaag 240  
 |||||  
 Sbjct: 181 cccaaggctgttggtgttttagaggtgctatctccagttccttgcaactcctgttaacaag 240

Query: 241 cacctcagcgagagcagcagcagcgatagcagccgcagaagagccagcggggtcgcttag 300  
 |||||  
 Sbjct: 241 cacctcagcgagagcagcagcagcgatagcagccgcagaagagccagcggggtcgcttag 300

Query: 301 tgtcatgaccagggcgaggagatcacaaccgccagagaggatgctgtggatccttggccga 360  
 |||||  
 Sbjct: 301 tgtcatgaccagggcgaggagatcacaaccgccagagaggatgctgtggatccttggccga 360

Query: 361 ctacctgacctctgcaaaattccttctctaccttggtc 398  
 |||||  
 Sbjct: 361 ctacctgacctctgcaaaattccttctctaccttggtc 398



Entrez

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

Back

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History

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Display

Show:

Send to

1: [AF226614](#). Homo sapiens ferr...[gi:7109248][Links](#)

LOCUS AF226614 2222 bp mRNA linear PRI 29-FEB-2000  
 DEFINITION Homo sapiens ferroportin1 (FPN1) mRNA, complete cds.  
 ACCESSION AF226614  
 VERSION AF226614.1 GI:7109248  
 KEYWORDS .  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2222)  
 AUTHORS Donovan,A., Brownlie,A., Zhou,Y., Shepard,J., Pratt,S.J.,  
 Moynihan,J., Paw,B.H., Drejer,A., Barut,B., Zapata,A., Law,T.C.,  
 Brugnara,C., Lux,S.E., Pinkus,G.S., Pinkus,J.L., Kingsley,P.D.,  
 Palis,J., Fleming,M.D., Andrews,N.C. and Zon,L.I.  
 TITLE Positional cloning of zebrafish ferroportin1 identifies a conserved  
 vertebrate iron exporter  
 JOURNAL Nature 403 (6771), 776-781 (2000)  
 MEDLINE [2015474](#)  
 PUBMED [10693807](#)  
 REFERENCE 2 (bases 1 to 2222)  
 AUTHORS Donovan,A., Brownlie,A., Shepard,J., Pratt,S.J., Paw,B.H., Barut,B.  
 and Zon,L.I.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-JAN-2000) Hematology/Oncology, Children's Hospital,  
 300 Longwood Ave., Boston, MA 02115, USA  
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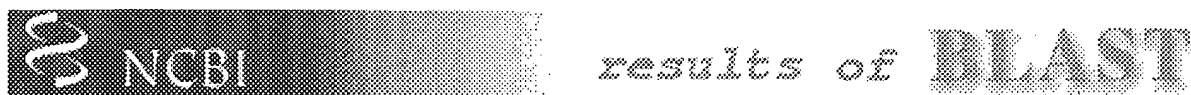
## ORIGIN

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2221 aa
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//

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[NCBI](#) | [NLM](#) | [NIH](#)

Oct 29 2003 07:23:28



# BLASTN 2.2.6 [Apr-09-2003]

RID: 1067977127-36-2085302.BLASTQ3

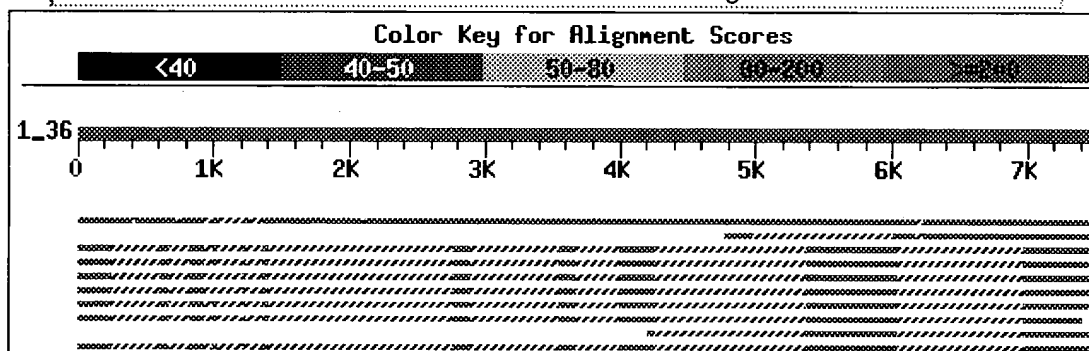
Query= *7-Genomiz*  
(7496 letters)

**Database:** All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)  
1,962,268 sequences; 9,398,544,397 total letters

Taxonomy reports

## Distribution of 211 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:

	Score	E
	(bits)	Value

<a href="#">gi 13270751 gb AC013439.11 </a> Homo sapiens BAC clone RP11-270...	<a href="#">2589</a>	0.0 <b>98</b>
<a href="#">gi 31873559 emb BX537503.1 HSM805934</a> Homo sapiens mRNA; cDN...	<a href="#">2260</a>	0.0 <b>98</b>
<a href="#">gi 22902429 gb BC037733.1 </a> Homo sapiens solute carrier fami...	<a href="#">1273</a>	0.0 <b>100</b>
<a href="#">gi 31543639 ref NM_014585.3 </a> Homo sapiens solute carrier fa...	<a href="#">1273</a>	0.0 <b>100</b>
<a href="#">gi 7109248 gb AF226614.1 AF226614</a> Homo sapiens ferroportin1...	<a href="#">1273</a>	0.0 <b>100</b>
<a href="#">gi 12053382 emb AL136944.1 HSM801908</a> Homo sapiens mRNA; cDN...	<a href="#">1273</a>	0.0 <b>100</b>
<a href="#">gi 23273531 gb BC035893.1 </a> Homo sapiens solute carrier fami...	<a href="#">1265</a>	0.0 <b>100</b>
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<a href="#">gi 7023677 dbj AK002038.1 </a> Homo sapiens cDNA FLJ11176 fis, ...	<a href="#">1251</a>	0.0 <b>100</b>
<a href="#">gi 8895484 gb AF215636.1 AF215636</a> Homo sapiens SLC11A3 iron...	<a href="#">1241</a>	0.0 <b>100</b>

Alignments

Deselect all

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Strand = Plus / Minus

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Sbjct: 136099 ttataactgtattcacctgactattataattttgtattatgtgtactacagatgatcta 136040

Query: 3342 gatgatacaggtaggacattatgccattgactactggtattcattcagtttcatatct 3401  
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Query: 3582 atattgcaaatttgccagtagtactgcaatcacaatccaaagggattggattgttg 3641  
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Strand = Plus / Minus

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Query: 4265 tgaacacaatgatctctccttttgttctcatgttcagaccttaaatgttggtgaagatca 4324

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Sbjct: 129219 atcgctttggttagacgaggcaagagcaggcttttgaggatctagggaactccgggtt 129160

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Query: 4505 agaggttcaattttacttgagagatagctgggcaaagctaagtcataggactgggaaaaa 4564  
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Sbjct: 129099 agaggttcaattttacttgagagatagctgggcaaagctaagtcataggactgggaaaaa 129040

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Sbjct: 129039 atgtggggaaaaaaagagaatgagagaatcccttgactctgtgaggaggagttatgta 128980

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Sbjct: 128919 aggacgctgggcttctgggtaaacagaatcttttatccagctctgcagggacccagaaaa 128860

Query: 4744 taatatgctggttg 4757  
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Sbjct: 128859 taatatgctggttg 128846

Score = 1513 bits (763), Expect = 0.0  
Identities = 835/855 (97%), Gaps = 3/855 (0%)  
Strand = Plus / Minus

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Sbjct: 137614 atcatctgcctactgagtggcagagaaaaggctaccaggtgtctttatctgtccttactc 137555

Query: 2174 cagtgcctttatctatatgggcgccctcataagagagttgccatctgtgatgaaagggg-ag 2232  
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Sbjct: 137554 cagtgcctttatctatatgggcgccctcataagagaattgccatctgtgatggaaggggtag 137495

Query: 2233 cttagaatttcgtagcaatggcaaatagcgtagtatgcaaagaaataccctgctgcttt 2292  
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Sbjct: 137494 cttagaatttcgtagcaatggcaaatagcattagtagtatgcaaagaaatacactgctgcttt 137435

Query: 2293 attctgggcaaatttttgtgtgtcttttctatttaggtaagccatattatcagattcagc 2352  
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Sbjct: 137434 attctgggcaaatttttgtgtgtcttttctatttaggtaaacatattatcagattcagc 137375

Query: 2353 ctgccatgtaggaggttgttaggtttgataacttcctctttaacctcatacatgttattgt 2412  
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Sbjct: 137374 ctgccatgtaggaggttgttagatttcataacttcctctttaacctcatacatgttattgt 137315

Query: 2413 tttaccttaagcaacaaagagctgaaatgtggatcatgtctatatcatactacagctcca 2472  
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Sbjct: 137314 tttaccttaagcaacaaagagctgaaatgtggatcatgtctatatcatactacagctcca 137255

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Sbjct: 137254 tttatgttaaactttcaagaagataaaactaaatgaaaatgtagtcattatgatagacttc 137195

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Query: 2593 gatcctctgggttgattgagagtagttgaggcaggactgacttcagaaagggttttcttt 2652  
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Sbjct: 137134 gatcctctgggttgattgagagtagttgaggcaggactgacttcagaaagggttttcttt 137075

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Sbjct: 137074 ttatctggtaataattaggtctgtgtattaatgtattatagtagaacaattatgtgtgga 137015

Query: 2713 taagagcagtctcagttagccattttgatgtaatgtacactttctctcttctctgcaca 2772  
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Sbjct: 137014 taagaacagtctcactgagacattttgatgtaatgtacactttctctcttctctgcaca 136955

Query: 2773 gtggcccagacctcgctggtggtacagaatgtttcagtcacacctgtgtggaatcatcctg 2832  
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Sbjct: 136954 gtggcccagacctcgctggtggtacagaatgtttcagtcacacctgtgtggaatcatcctg 136895

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Sbjct: 136894 atgatggttttcttacataaacatgagcttctgaccatgtaccatggatgggttctcgta 136835

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Sbjct: 136774 aatgctttgaagcta 136760

Score = 1324 bits (668), Expect = 0.0  
Identities = 718/733 (97%), Gaps = 3/733 (0%)  
Strand = Plus / Minus

Query: 1361 tcggtgactgggtggacaagaatgctagacttaaaggtagtggttattataattaatc 1420  
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Sbjct: 139068 gagagaaacaaccagggaatgtctgcatgccacacttgaggaggagggttagatggca 139009

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Sbjct: 139008 ccacctctggatggagggtcccatggctccacacaaagttgggatgcctggacattgac 138949

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Query: 1841 tcaaggcagaatagttgagcctggatcaciaagagctgaattataaattttgtagggaaa 1900  
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Sbjct: 138529 atgatcattcagggttaaattttcttgaattgctcagttgataat-gccaag-acctgacc 138472

Query: 2081 atgcctgacttag 2093  
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Sbjct: 138471 atgcctgacttag 138459

Score = 347 bits (175), Expect = 2e-91  
Identities = 235/255 (92%)  
Strand = Plus / Minus

Query: 4788 ctgttgcccaggctgaagtgcagtgggcgcatcttggtcactgcaagctctgcctcctg 4847  
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Query: 4848 gggtcacgccattctcctgcctcagcctcccaagtagctgggattgcaggcatccaccac 4907  
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Identities = 239/266 (89%), Gaps = 3/266 (1%)  
Strand = Plus / Minus

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Sbjct: 16471 cgccattctcctgcctcagcctcccaagtagctgggactacaggtgcctgccaccatacc 16412

Query: 4914 cggctaattttttgtatttt---tagtagagacgggggtttcaccatgtagccaggatgg 4970

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Score = 283 bits (143), Expect = 2e-72

Identities = 240/271 (88%), Gaps = 1/271 (0%)

Strand = Plus / Minus

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Identities = 215/241 (89%), Gaps = 2/241 (0%)

Strand = Plus / Plus

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11/4/03



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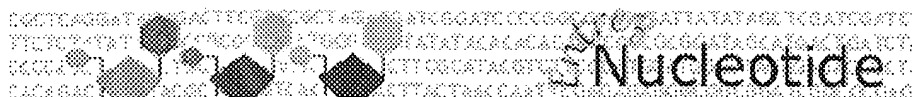
Score = 218 bits (110), Expect = 1e-52  
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Strand = Plus / Minus

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Query: 4875 tcccaagtagctgggattgcaggcatccaccaccacacccggctaattttttgtattttt 4934

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Entrez

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Nucleotide

Protein

Genome

Structure

PMC

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Details

Display

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Send to

☐ 1: [AF231121](#). Homo sapiens iron...[gi:7264728][Links](#)

LOCUS AF231121 2443 bp mRNA linear PRI 20-MAR-2000

DEFINITION Homo sapiens iron-regulated transporter IREG1 (IREG1) mRNA, complete cds.

ACCESSION AF231121

VERSION AF231121.1 GI:7264728

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM [Homo sapiens](#)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2443)

AUTHORS McKie,A.T., Marciani,P., Rolfs,A., Brennan,K., Wehr,K., Barrow,D., Miret,S., Bomford,A., Peters,T.J., Farzaneh,F., Hediger,M.A., Hentze,M.W. and Simpson,R.J.

TITLE A novel duodenal iron-regulated transporter, IREG1, implicated in the basolateral transfer of iron to the circulation

JOURNAL Mol. Cell 5 (2), 299-309 (2000)

MEDLINE [20337919](#)

PUBMED [10882071](#)

REFERENCE 2 (bases 1 to 2443)

AUTHORS McKie,A.T.

TITLE Direct Submission

JOURNAL Submitted (02-FEB-2000) Molecular Medicine, King's College London, Guy's, King's and St. Thomas' Medical School, Rayne Institute 123 Coldharbour Lane, London SE5 9NU, UK

FEATURES

source Location/Qualifiers

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/gene="IREG1"

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CDS 305..2020

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## ORIGIN

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2281 tcccctatct ctcagtagta gatacaatct tacgtaaaaag agtgggttagt cacgtgaatt
2341 cagttatcat ttgacagatt cttatctgta ctagaattca gatatgtcag ttttctgcaa
2401 aactcactct tgttcaagac tagctaattt atttttttgc atc
```

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